

Serial Number: 09/869,334CRF Processing Date 10/4/2001Edited by JSVerified by JS

(STIC stat

**ENTERED**☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_☐

Added the mandatory heading and subheadings for "Current Application Data"

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☐Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lastname at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_☐

Inserted mandatory headings, specifically: \_\_\_\_\_

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

☒

Other:

Deleted extra headings

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form

3/1/95

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,334

DATE: 10/04/2001

TIME: 12:48:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I869334.raw

```

4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
6 <120> TITLE OF INVENTION: A Process for producing HMG-CoA Reductase inhibitor
8 <130> FILE REFERENCE: H11-0011T4
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/869,334
C--> 10 <141> CURRENT FILING DATE: 2001-07-14
10 <160> NUMBER OF SEQ ID NOS: 45
12 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 396
16 <212> TYPE: PRT
17 <213> ORGANISM: Bacillus subtilis
19 <400> SEQUENCE: 1
20 Met Asn Val Leu Asn Arg Arg Gln Ala Leu Gln Arg Ala Leu Leu Asn
21 1 5 10 15
23 Gly Lys Asn Lys Gln Asp Ala Tyr His Pro Phe Pro Trp Tyr Glu Ser
24 20 25 30
26 Met Arg Lys Asp Ala Pro Val Ser Phe Asp Glu Glu Asn Gln Val Trp
27 35 40 45
29 Ser Val Phe Leu Tyr Asp Asp Val Lys Lys Val Val Gly Asp Lys Glu
30 50 55 60
32 Leu Phe Ser Ser Cys Met Pro Gln Gln Thr Ser Ser Ile Gly Asn Ser
33 65 70 75 80
35 Ile Ile Asn Met Asp Pro Pro Lys His Thr Lys Ile Arg Ser Val Val
36 85 90 95
38 Asn Lys Ala Phe Thr Pro Arg Val Met Lys Gln Trp Glu Pro Arg Ile
39 100 105 110
41 Gln Glu Ile Thr Asp Glu Leu Ile Gln Lys Phe Gln Gly Arg Ser Glu
42 115 120 125
44 Phe Asp Leu Val His Asp Phe Ser Tyr Pro Leu Pro Val Ile Val Ile
45 130 135 140
47 Ser Glu Leu Leu Gly Val Pro Ser Ala His Met Glu Gln Phe Lys Ala
48 145 150 155 160
50 Trp Ser Asp Leu Leu Val Ser Thr Pro Lys Asp Lys Ser Glu Glu Ala
51 165 170 175
53 Glu Lys Ala Phe Leu Glu Glu Arg Asp Lys Cys Glu Glu Glu Leu Ala
54 180 185 190
56 Ala Phe Phe Ala Gly Ile Ile Glu Glu Lys Arg Asn Lys Pro Glu Gln
57 195 200 205
59 Asp Ile Ile Ser Ile Leu Val Glu Ala Glu Glu Thr Gly Glu Lys Leu
60 210 215 220
62 Ser Gly Glu Glu Leu Ile Pro Phe Cys Thr Leu Leu Leu Val Ala Gly
63 225 230 235 240
65 Asn Glu Thr Thr Thr Asn Leu Ile Ser Asn Ala Met Tyr Ser Ile Leu
66 245 250 255
68 Glu Thr Pro Gly Val Tyr Glu Glu Leu Arg Ser His Pro Glu Leu Met
69 260 265 270
71 Pro Gln Ala Val Glu Glu Ala Leu Arg Phe Arg Ala Pro Ala Pro Val

```

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```

72          275          280          285
74 Leu Arg Arg Ile Ala Lys Arg Asp Thr Glu Ile Gly Gly His Leu Ile
75          290          295          300
77 Lys Glu Gly Asp Met Val Leu Ala Phe Val Ala Ser Ala Asn Arg Asp
78 305          310          315          320
80 Glu Ala Lys Phe Asp Arg Pro His Met Phe Asp Ile Arg Arg His Pro
81          325          330          335
83 Asn Pro His Ile Ala Phe Gly His Gly Ile His Phe Cys Leu Gly Ala
84          340          345          350
86 Pro Leu Ala Arg Leu Glu Ala Asn Ile Ala Leu Thr Ser Leu Ile Ser
87          355          360          365
89 Ala Phe Pro His Met Glu Cys Val Ser Ile Thr Pro Ile Glu Asn Ser
90          370          375          380
92 Val Ile Tyr Gly Leu Lys Ser Phe Arg Val Lys Met
93 385          390          395
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 1191
98 <212> TYPE: DNA
99 <213> ORGANISM: Bacillus subtilis
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (1)..(1191)
105 <400> SEQUENCE: 2
106 atg aat gtg tta aac cgc cgg caa gcc ttg cag cga gcg ctg ctc aat 48
107 Met Asn Val Leu Asn Arg Arg Gln Ala Leu Gln Arg Ala Leu Leu Asn
108 1          5          10          15
110 ggg aaa aac aaa cag gat gcg tat cat ccg ttt cca tgg tat gaa tcg 96
111 Gly Lys Asn Lys Gln Asp Ala Tyr His Pro Phe Pro Trp Tyr Glu Ser
112          20          25          30
114 atg aga aag gat gcg cct gtt tcc ttt gat gaa gaa aac caa gtg tgg 144
115 Met Arg Lys Asp Ala Pro Val Ser Phe Asp Glu Glu Asn Gln Val Trp
116          35          40          45
118 agc gtt ttt ctt tat gat gat gtc aaa aaa gtt gtt ggg gat aaa gag 192
119 Ser Val Phe Leu Tyr Asp Asp Val Lys Lys Val Val Gly Asp Lys Glu
120          50          55          60
122 ttg ttt tcc agt tgc atg ccg cag cag aca agc tct att gga aat tcc 240
123 Leu Phe Ser Ser Cys Met Pro Gln Gln Thr Ser Ser Ile Gly Asn Ser
124 65          70          75          80
126 atc att aac atg gac ccg ccg aag cat aca aaa atc cgt tca gtc gtg 288
127 Ile Ile Asn Met Asp Pro Pro Lys His Thr Lys Ile Arg Ser Val Val
128          85          90          95
130 aac aaa gcc ttt act ccg cgc gtg atg aag caa tgg gaa ccg aga att 336
131 Asn Lys Ala Phe Thr Pro Arg Val Met Lys Gln Trp Glu Pro Arg Ile
132          100          105          110
134 caa gaa atc aca gat gaa ctg att caa aaa ttt cag ggg cgc agt gag 384
135 Gln Glu Ile Thr Asp Glu Leu Ile Gln Lys Phe Gln Gly Arg Ser Glu
136          115          120          125
138 ttt gac ctt gtt cac gat ttt tca tac ccg ctt ccg gtt att gtg ata 432
139 Phe Asp Leu Val His Asp Phe Ser Tyr Pro Leu Pro Val Ile Val Ile

```

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```

140      130      135      140
142 tct gag ctg ctg gga gtg cct tca gcg cat atg gaa cag ttt aaa gca 480
143 Ser Glu Leu Leu Gly Val Pro Ser Ala His Met Glu Gln Phe Lys Ala
144 145      150      155      160
146 tgg tct gat ctt ctg gtc agt aca ccg aag gat aaa agt gaa gaa gct 528
147 Trp Ser Asp Leu Leu Val Ser Thr Pro Lys Asp Lys Ser Glu Glu Ala
148      165      170      175
150 gaa aaa gcc ttt ttg gaa gaa cga gat aag tgt gag gaa gaa ctg gcc 576
151 Glu Lys Ala Phe Leu Glu Glu Arg Asp Lys Cys Glu Glu Glu Leu Ala
152      180      185      190
154 gcg ttt ttt gcc ggc atc ata gaa gaa aag cga aac aaa ccg gaa cag 624
155 Ala Phe Phe Ala Gly Ile Ile Glu Glu Lys Arg Asn Lys Pro Glu Gln
156      195      200      205
158 gat att att tct att tta gtg gaa gcg gaa gaa aca ggc gag aag ctg 672
159 Asp Ile Ile Ser Ile Leu Val Glu Ala Glu Glu Thr Gly Glu Lys Leu
160      210      215      220
162 tcc ggt gaa gag ctg att ccg ttt tgc acg ctg ctg ctg gtg gcc gga 720
163 Ser Gly Glu Glu Leu Ile Pro Phe Cys Thr Leu Leu Leu Val Ala Gly
164 225      230      235      240
166 aat gaa acc act aca aac ctg att tca aat gcg atg tac agc ata tta 768
167 Asn Glu Thr Thr Thr Asn Leu Ile Ser Asn Ala Met Tyr Ser Ile Leu
168      245      250      255
170 gaa acg cca ggc gtt tac gag gaa ctg cgc agc cat cct gaa ctg atg 816
171 Glu Thr Pro Gly Val Tyr Glu Glu Leu Arg Ser His Pro Glu Leu Met
172      260      265      270
174 cct cag gca gtg gag gaa gcc ttg cgt ttc aga gcg ccg gcc ccg gtt 864
175 Pro Gln Ala Val Glu Glu Ala Leu Arg Phe Arg Ala Pro Ala Pro Val
176      275      280      285
178 ttg agg cgc att gcc aag cgg gat acg gag atc ggg ggg cac ctg att 912
179 Leu Arg Arg Ile Ala Lys Arg Asp Thr Glu Ile Gly Gly His Leu Ile
180      290      295      300
182 aaa gaa ggt gat atg gtt ttg gcg ttt gtg gca tcg gca aat cgt gat 960
183 Lys Glu Gly Asp Met Val Leu Ala Phe Val Ala Ser Ala Asn Arg Asp
184 305      310      315      320
186 gaa gca aag ttt gac aga ccg cac atg ttt gat atc cgc cgc cat ccc 1008
187 Glu Ala Lys Phe Asp Arg Pro His Met Phe Asp Ile Arg Arg His Pro
188      325      330      335
190 aat ccg cat att gcg ttt ggc cac ggc atc cat ttt tgc ctt ggg gcc 1056
191 Asn Pro His Ile Ala Phe Gly His Gly Ile His Phe Cys Leu Gly Ala
192      340      345      350
194 ccg ctt gcc cgt ctt gaa gca aat atc gcg tta acg tct ttg att tct 1104
195 Pro Leu Ala Arg Leu Glu Ala Asn Ile Ala Leu Thr Ser Leu Ile Ser
196      355      360      365
198 gct ttt cct cat atg gag tgc gtc agt atc act ccg att gaa aac agt 1152
199 Ala Phe Pro His Met Glu Cys Val Ser Ile Thr Pro Ile Glu Asn Ser
200      370      375      380
202 gtg ata tac gga tta aag agc ttc cgt gtg aaa atg taa 1191
203 Val Ile Tyr Gly Leu Lys Ser Phe Arg Val Lys Met
204 385      390      395

```

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I869334.raw

207 <210> SEQ ID NO: 3  
208 <211> LENGTH: 39  
209 <212> TYPE: DNA  
210 <213> ORGANISM: Artificial Sequence  
212 <220> FEATURE:  
213 <223> OTHER INFORMATION: Synthetic DNA  
215 <400> SEQUENCE: 3  
216 tttggatccg aattcaaaag tgctggcgct gttccgttt 39  
219 <210> SEQ ID NO: 4  
220 <211> LENGTH: 41  
221 <212> TYPE: DNA  
222 <213> ORGANISM: Artificial Sequence  
224 <220> FEATURE:  
225 <223> OTHER INFORMATION: Synthetic DNA  
227 <400> SEQUENCE: 4  
228 gtgggatccg tcgaccactt ttttcacgat gttcactccc c 41  
231 <210> SEQ ID NO: 5  
232 <211> LENGTH: 39  
233 <212> TYPE: DNA  
234 <213> ORGANISM: Artificial Sequence  
236 <220> FEATURE:  
237 <223> OTHER INFORMATION: Synthetic DNA  
239 <400> SEQUENCE: 5  
240 ccaggatcct ctagatgggtg aaatggttgt tgccgctct 39  
243 <210> SEQ ID NO: 6  
244 <211> LENGTH: 39  
245 <212> TYPE: DNA  
246 <213> ORGANISM: Artificial Sequence  
248 <220> FEATURE:  
249 <223> OTHER INFORMATION: Synthetic DNA  
251 <400> SEQUENCE: 6  
252 tcaggatccc ccgggtgagc ggcaaatcca cccaccctg 39  
255 <210> SEQ ID NO: 7  
256 <211> LENGTH: 37  
257 <212> TYPE: DNA  
258 <213> ORGANISM: Artificial Sequence  
260 <220> FEATURE:  
261 <223> OTHER INFORMATION: Synthetic DNA  
263 <400> SEQUENCE: 7  
264 taagcgcgcc ccgggttaat tggatgggcy aaagctc 37  
267 <210> SEQ ID NO: 8  
268 <211> LENGTH: 39  
269 <212> TYPE: DNA  
270 <213> ORGANISM: Artificial Sequence  
272 <220> FEATURE:  
273 <223> OTHER INFORMATION: Synthetic DNA  
275 <400> SEQUENCE: 8  
276 atcgcgcgcg tcgacgatag cggcagaaaa ttggcggca 39  
279 <210> SEQ ID NO: 9

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I869334.raw

```

280 <211> LENGTH: 38
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Synthetic DNA
287 <400> SEQUENCE: 9
288 agcggatccg aattcgctgg aatcaaaagt cggccaga      38
291 <210> SEQ ID NO: 10
292 <211> LENGTH: 38
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Synthetic DNA
299 <400> SEQUENCE: 10
300 tcaggatccg tcgactgaga aaacacaaac gccccctc      38
303 <210> SEQ ID NO: 11
304 <211> LENGTH: 39
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic DNA
311 <400> SEQUENCE: 11
312 atgggatacct ctagacatgt tgtagtttgg gttggaatc      39
315 <210> SEQ ID NO: 12
316 <211> LENGTH: 42
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Synthetic DNA
323 <400> SEQUENCE: 12
324 gccggatcca gatctggcat cacacaacaa taaatacacc gc      42
327 <210> SEQ ID NO: 13
328 <211> LENGTH: 39
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Synthetic DNA
335 <400> SEQUENCE: 13
336 tctggatacct ctagaagaga acacaaagag tacgaatgc      39
339 <210> SEQ ID NO: 14
340 <211> LENGTH: 41
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Synthetic DNA
347 <400> SEQUENCE: 14
348 aaaggatccc ccgggtttac cagccagcgc aacaaagtca t      41
351 <210> SEQ ID NO: 15
352 <211> LENGTH: 39

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/869,334

DATE: 10/04/2001

TIME: 12:48:36

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I869334.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:699 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:703 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:707 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:711 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:719 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:723 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:731 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:735 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:743 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:795 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:1001 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
L:1002 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44

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Input Set : A:\PTO.AMC.txt

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L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44